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1	ATTTTATTACCAATCTTATATAATTAAATTCTCTTACAAAAATCTCTAAATG	60
61	TTTTTACCTAATATATATCTGGCTGTATCTACTTGCACCTCCACTATGTTAAT	120
121	TTTATTTCACATTAGGTGTAATAATGAATTGCAAAAAATTCTTATAACAAACTGCATT	180
	<u>M N C K I L I T T A L</u>	
181	AATATCATTAAATGTACTCTATTCCAAGCATATCTTTCTGATACTATAAAGATGGTAA	240
	<u>I S L M Y S I P S I S F Y V P S D T I Q D G N</u>	
241	CATGGGTGTTAACTTCTTATAGTGGAAAGTATGTACCAAGTGTCTCACATTGGTAG	300
	<u>M G G N F Y I S G K Y V P S V S H F G S</u>	
301	CTTCTCAGCTAAAGAAGAAACTCAAATGTTGGAGTTGGATTAAACATGATTG	360
	<u>F S A K E S K S T V G V F G L K H D W</u>	
361	GGATGGAAGTCCAATACTTAAGAATAAACACGGCTGACTTTACTGTTCCAAACTATTGTT	420
	<u>D G S P I L K N K H A D F T V P N Y S F</u>	
421	CAGATACGAGAACAAATTCCATTCTAGGGTTAGGGAGCTATCGGTTACTCAATGGGTGG	480
	<u>R Y E N N P F L G F A G Y S M G G</u>	
481	CCCAAGAAATAGAATTCTTATGAGCGATTGGCTAAAGTCCTAAATCAA	540
	<u>P R I E F E I S Y E A F D V K S P N I N</u>	
541	TTATCAAATGACGGCACAGGTACTGGCTCTATCTCATCACACATGGCAGCCATGGA	600
	<u>Y Q N D A H R Y C A L S H H T S A A M E</u>	
601	AGCTGATAATTGTCTTCTTAAAGAACGAAAGGGTTAATTGACATATCACTTGCATAAAA	660
	<u>A D K F V F L K N E G L I D I S L A I N</u>	
661	TGCATGTTATGATAATAATGACAAAGTACCTGTTCTCCATTATATGCGCAGGTAT	720
	<u>A C Y D I I N D K V P V S P Y I C A G T I</u>	

Fig. 1A

721 TGGTACTGATTGATTCTATGTTGAAGCTACAAGTCCTAAAATTCCCTACCAAGGAAA 780
 G T D L I S M F E A T S P K I S Y Q G K

 841 CAGGATCATAGGTAATGAGTTAGAGATATTCTGCAATAGTACCTAGTAACCTAACTAC 900
 R I G N E F R D I P A I V P S N S T T

 901 ATAAGTGGACCAATTGCAACAGTAACACTAAATGTTGACTTGGTTAGAACT 960
 I S G P Q F A T V T L N V C H F G L E L

 961 TGGAGGAAGATTAACTTAACTTATTGTTGCCACATATTAAAATGATCTAACTTG 1020
 G G R F N F (SEQ. ID NO: 2)

 1021 TTTTAWTATTGCTACATACAAAAAAAGAAAAAATAGTGGCAAAAGAAATGTAGCAATAAGA 1080
 1081 GGGGGGGGGGGGACCAATTATCTTCTATGCTTCCCCAAAGTTTTCYCGCTATTATGA 1140
 1141 CTTAACAAACAGAAGGTAATACTCCTCACGGAAAACCTTACAAATTTTAAATTATA 1200
 1201 CCAACTTATATAATATAATTAAATTCTTACAAAATCACTAGTATTACCAAAA 1260
 1261 TATATAATTCTGACTTGTCTTCTGCACTTCTACTATTAAATTATTTGTCACTAT 1320
 1321 TAGGTATAATAAWATGAATTGCMAAAGATTTCATAGCAAGTGCATTGATTCACTAA 1380
 1381 TGTCTTCTTACCTAGCGTATCTGAATTACATGAAGATAATAATGGTA 1440
 1441 ACTTTACATTAGTGCAGGAAAGTATAATGCCAAGTGCCTCACACTTGGCGTATTTCAGTAA 1500
 1501 AAGAAGAGAAAACACAAACAAACTGGAGTTTGGATTAAACAAAGATTGGACGGCAA 1560
 1561 CACTAAAGGATGCAAGCWGCAACACACAWTAGACCCAAAGTACAATG 1607

(SEQ ID NO: 1)

Fig. 1.B

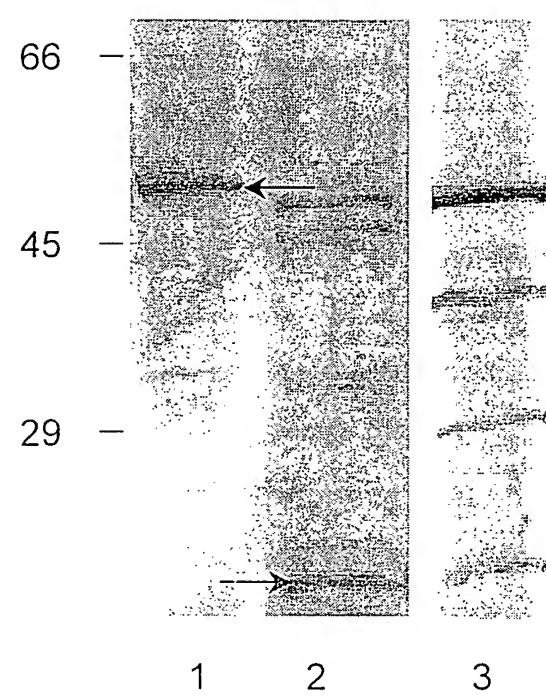


Fig. 2

ECaP28 MNCKKILITLISIPLMYSIPSISFTDIQDGNG-GN----FYISGKVVPSVSHFGSESAKE----ESKSTVGVFGLKHH 70
 ECa28SA2 ...VFTIS...SI.FL.NV.Y.NPVYGNs.-Y...M...P...I...E...K.K.TV.Y...E 70
 ECa28SA1 .KY...TFTV...VL.TSFTHF.P.YSPARASTIH--...M...TA...I...QSF.KVLV..DQ 69
 EChP28 .Y...VF...S...IS.L.GV...PA-GSGIN...M...A...V...RNT...Q 69
 OMP-1B ...Y...FVSS...SIL.YQ.A.PVTSNDT.INDSREG...V...N...I...RK...E.APINGNTSI.KK...K 80
 OMP-1C ...FF...ALP.SEL.G.LL.EPV..DSVS...M...A...V...KNP..ALY...Q 70
 OMP-1D ...E.FF...TL..SFL.G..L..PV..D.IS...M...A...V...RNT...IEQ 70
 OMP-1E ...FF...V...SFL.G...PV.GD.IS...V...M...A...M...KNP..ALY...Q 70
 OMP-1F ...FF...T.V...SFL.G...AV.ND.V...V...Q...RNT.T...Q 70
 MAP-1 ...F...ST...VSFL.GV...V.EE.NPV.S----V...A..M.TA...KM.I...D.RD.KA...K 71

↓

VR1

ECaP28 DWDGSPILKNNKHAD-FTVPNYSFRYENNPFLGFAGAIGYSMGGPRIEFEISYEAFDVKSPNINYQNDAH--RYCALSH-- 145
 ECa28SA2 N.A.DA.SSQSPD.N..IR...K.AS.K...V...I.S...V.M...V.M...NQGN. (SEQ ID NO: 7) 133
 ECa28SA1 RLSHNI.NN.DT.KSLK.Q...K.K...I.NS..L.V.H.I.T.N.GN..L..S.--K...GS 147
 EChP28 N...A.SNSSPN.V...S...K...D...L.V...T...NQGN..K.E...-- 145
 OMP-1B ...GDIAQSAN.NRTDPALEFQ..LIS...S.S...A.D...L.AA.QK..A.N.DN.DT.SGDYYK.FG..RED 154
 OMP-1C ...N.-VSASSHADAD.NNKG...K...V...T...NQGG..K...V...T...DR-- 145
 OMP-1D ...RCV.SRTTLS.I...K...L.S...D...L.V...NQGN..K.E...Y...-- 146
 OMP-1E ...E.-ISSSSHNDH.NNKG...K...V...V...T...NQGN..K...GQ-- 145
 OMP-1F ...T.S..SPENT.N...K...V...L.N...L.M...T...NQGN..K...--K.Y..T.-- 146
 MAP-1 ...VKTPSGNTNSI..ERD...K...V...N...V...T...RN.GG..K...--M...-- 145

VR2

Fig. 3A

ECaP28	-----HTSAAME-----ADKFVFLKNEGLIDISLAINACYDIINDKVPVSPYICAGIGTDLISMFEATSPKISYQGKLGISY	217
ECa28SA2	HICSDGNGSGDWYTAKT.....L.....L.V.FML.....TTE.M.F.....T.QN.....	133
ECa28SA1	-----NS.ADMSSASNN.....L..FML.....VVGEGI.F.....V.....N.....L..	227
EChP28	AI-----ADK.Y.V.....ITFM..MV.T.....TAEG..FI.A..V.A..NV.KDFNL.F.....I.....	219
OMP-1B	KA.ST---NAT.SHY.L.....L..ML.....VVSEGI.F.....V.....IN.....L..	222
OMP-1C	LLGTETQIDGAGSAS..I.....L.K.FML.....V.SEGI.F.....I.V.....IN.....L..	218
OMP-1D	QDNGS---IPKTS.Y.L..S...L..FML.....ESI.L.....V.....N.....L..	222
OMP-1E	NSGGKLSNAG.....L..ML.....V.SEGI.F.....V.....IN.....L..	218
OMP-1F	DT.SSSTAG.TTS.MV...N.T...ML.....ML.GM.....V.....V.VIN..N..L.....	220
MAP-1		219
VR3		
ECaP28	SINPETSVFIGGFHRIIGNEFRDIPA---IVPSNSTTISGPQQF-ATVVTLNVCHFGLLELGGRFNF	(SEQ ID NO:2)
ECa28SA2	T..SRV...A...KV.....KG..T---LL.DG.NIKVQQS---D.....I.S..F.	278
EChP28	S..A...KV.....T---I.TG..LAGKGNYP.I..I.D..I.....A.	133
OMP-1B	P.T..V.A...YY.GV...N.NK..VITPV.LEGAPQTTS---L..IDTGY..G.V.V..T.	287
OMP-1C	A..V...KVA.....ST---LKAFATPSSAATPDL...S.....V.....	281
OMP-1D	P.S..A...KV.....T---MI..E.ALAGKGNYP.I..D.FY..I.....QL	283
OMP-1E	A...KV.....T---LKAFATPSSS--ATPDL.I..S.....I.....	280
OMP-1F	S..A...V...KV.....T..LTGN-H.-TI..S.....V.....	286
MAP-1	A..I...V...K..ATSKVFTS.GNASSAVSPGF.SAI.D...I.I..V.	278
VR4		284

Fig. 3B

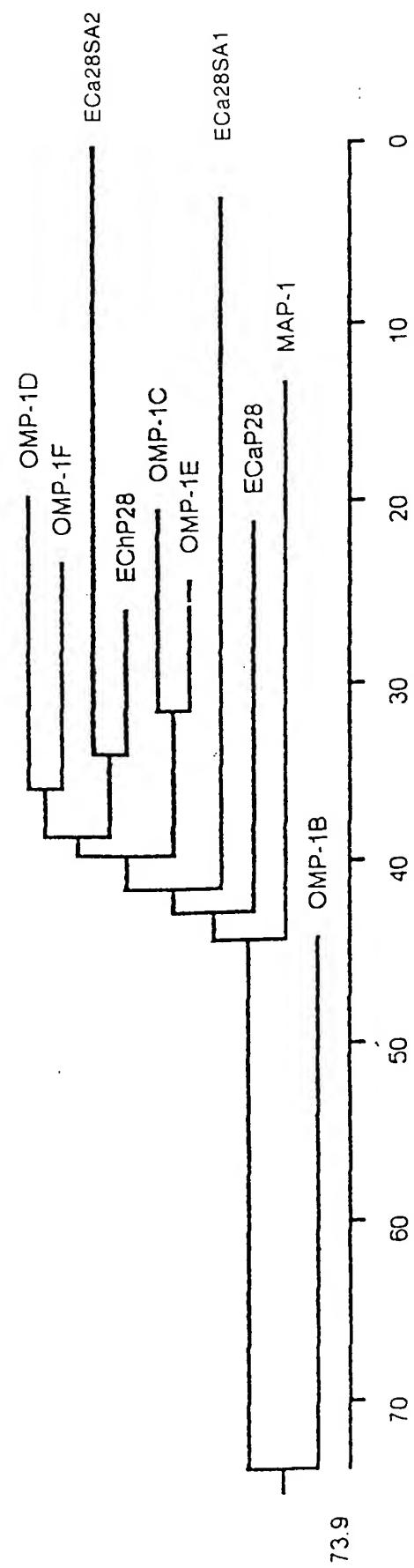


Fig. 4

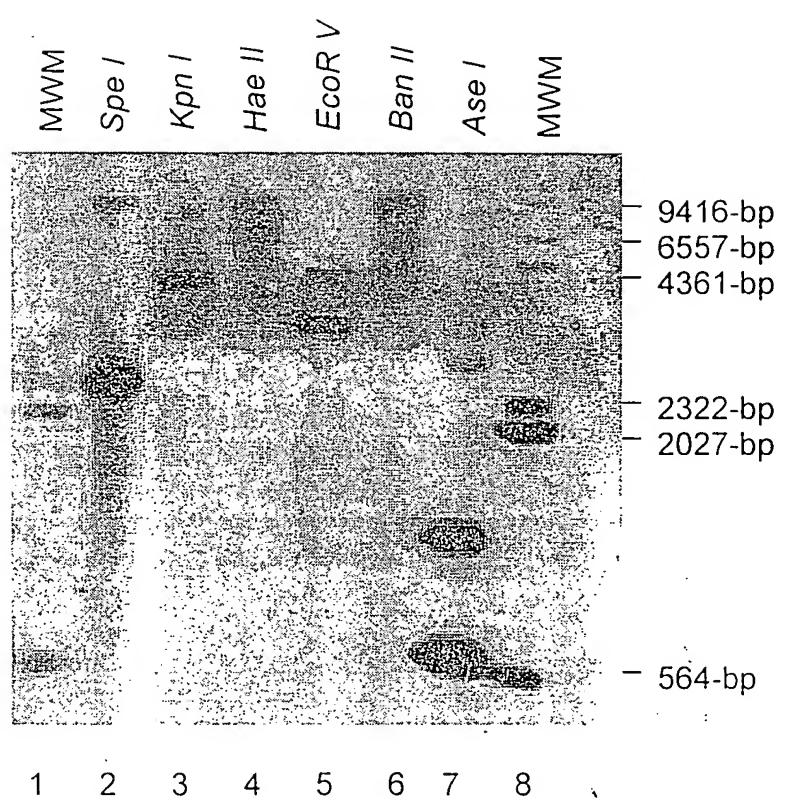
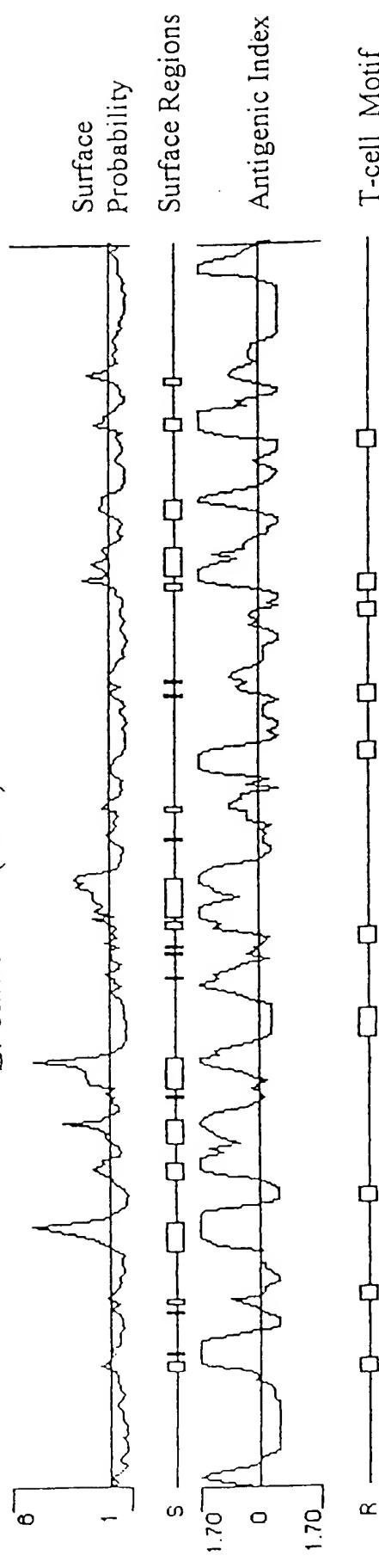


Fig. 5

E. canis P28 (Jake)



E. chaffeensis P28 (Arkansas)

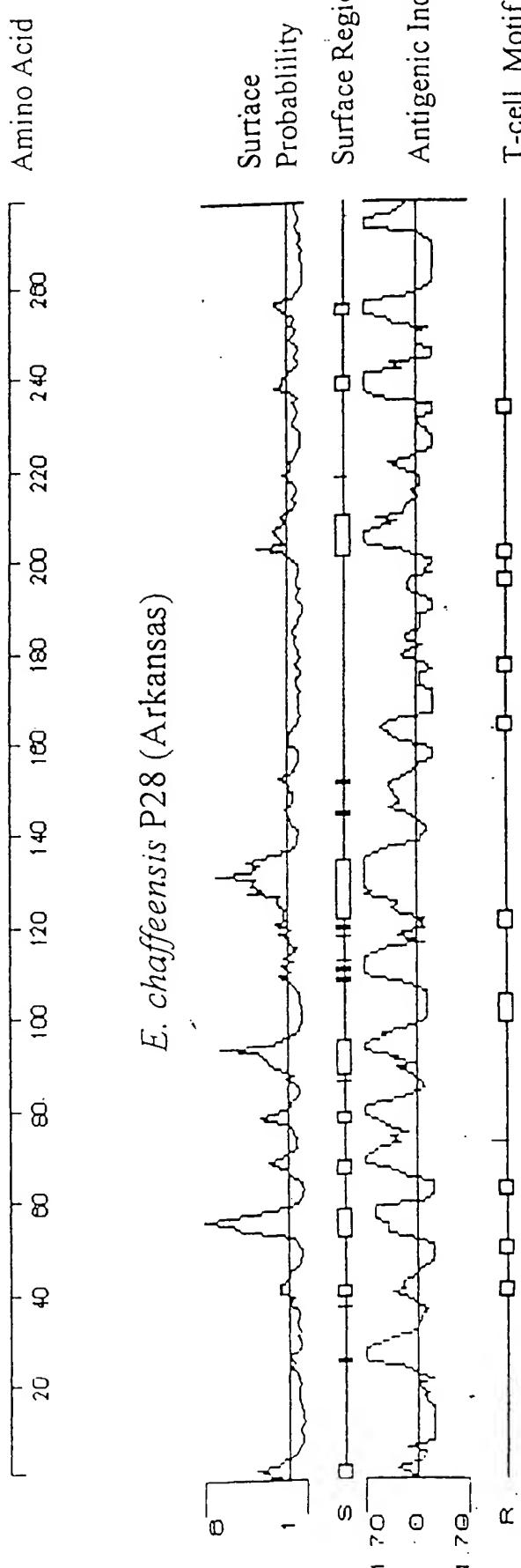


Fig. 6

Eca28SA2

ATGAAATTGTAAAAAGTTTCAAAATAAGTCATTGATATCATCCATTACTTCCCTACCT 60
M N C K V F T I S A L I S S I Y F L P

ATGTCTCATACTCTAACCCAGTATATGTAACAGTATGTATGGTAATTTCATATCA 120
N V S Y S N P V Y G N S M Y G N F Y I S

GGAAAGTACATGCCCAAGTGTCCCTCATTGGAAATTTCAGCTGAAGAAGAGAAAAAA 180
G K Y M P S V P H F G I F S A E E E K K

AGAGACAACGTAGTATATGGCTAAAGAAAACGGCAGGAGATGCAATATCTAGTCAA 240
K T T V V G L K E N W A G D A I S S Q

AGTCCAGATGATAATTACCATCGAAATTACTCATTCAGTATGCAAGCAACAAAGTT 300
S P D D N F T I R N Y S F K Y A S N K F

TAGGGTTGCAGTAGCTATTGGTTACTCGATAAGGCAGTCCAAGAATAGAAGTTGAGATG 360
L G F A V A I G Y S I G S P R I E V E M

TCTTATGAAAGCATTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTACAGG 420
S Y E A F D V K N P G D N Y K N G A Y R

TATTGTGCTTATCTCATCAAGATGATGCCGGATGACATGACTAGTGCACACTGACAAA 480
Y C A L S H Q D D A D D M T S A T D K

TTTGTATATTAAATTGAAGGATTACTTAACATATCATTTATGACAACATATGTTAT 540
F V Y L I N E G L L N I S F M T N I C Y

GAAACAGCAAGCAAAATATAACCTCTCTCCCTACATATGTGCAGGTATTGGTACTGAT 600
E T A S K N I P L S P Y I C A G I G T D

TTAATTCACATGTTGAAACTACACATCCTAAATTCTTATCAAGGAAAGCTAGGGTTG 660
L I H M F E T T H P K I S Y Q G K L G L

Fig. 7A

GCC TACT TCGTAAGTGCAGAGTCTCGGTTCTTTGGTATATTTCAAAAATTATA 720
 A Y F V S A E S V S F G I Y F H K I I

 AATAATAAGTTAAATAATGTTCCAGCCATGGTACCTATTAACTCAGACGAGATAGTAGGA 780
 N N K F K N V P A M V P I N S D E I V G

 CCACAGTTGCAACAGTAACATTAAATGTTGCTACTTTGGATTAGAAACTTGGATGTAGG 840
 P Q F A T V T L N V C Y F G L E L G C R

 (SEQ ID NO: 3)

 TTCAACTTCTAAATTTCGTGGTACACATATCACGAAGCTAAAAATTGTTTTATCTCTGC 900
 F N F * (SEQ ID NO: 4)

 TGTATACAGAGAAAAATAGTAGTAGTGAAATTACCTAACAAATATGACAGTACAAGTTAC 960
 CAAGCTTATTCTCACAAAACCTTCTGTGTCTTTATCTCTTACAATGAAATGTACACTT 1020
 AGCTTCACTACTGTAGAGTGTTTATCAATGCTTGTTTATTAAATACTCTACATAATAT 1080
 GTTAAATTCTTCTACAAAACACTAGTAAATTACTAGTAAATTACTAGAATAATTCTGACTTGT 1140

 (SEQ ID NO: 31)

Eca28SA3
 ATTGCTTTATACTTCCACTATTGTTAATTATTAGGTGTAATATGAAT 1200

 M N

 TGCAAAAAATTCTTATAACAACTGCATTAAATGTTACTATGCTCCAAAGCATA 1260
 C K I L I T A L M S L M Y A P S I

 TCTTTCTGATACTATAACAGGATAACACTGGTAGCTTCTACATCAGTGGAAATAT 1320
 S F S D T I Q D D N T G S F Y I S G K Y

 GTACCAAGTGTTCACATTGGTTCTCAGCTAAAGAAGAAACTCAACTGTT 1380
 V P S V S H F G V F S A K E E R N S T V

 GGAGTTTGGATTAAACATGATTGGAATGGGGTACAAATCTAACTCTCCAGAA 1440
 G V F G L K H D W N G G T I S N S P E

Fig. 7B

AATATATTACAGTTCAAATTATTTCGTTTAATACGAAAACAACCCATTCTTAGGGTTT 1500
 N I F T V Q N Y S F K Y E N N P F L G F

 GCAGGAGCTATTGGTTATTICAATGGGTGGCCCAAGAATAGAACTTGAAGTTCTGTACGAG 1560
 A G A I G Y S M G G P R I E L E V L Y E

 ACATTCGATGTGAAAAATTCAAAGAAATAATTATAGAACGGCGCACACAGATACTGTGCT 1620
 T F D V K N Q N N Y K N G A H R Y C A

 TTATCTCATCATAGTTAGCAACAAAGCATGTCCTCCGCAAGTAACAAATTGTGTTCTTA 1680
 L S H H S S A T S M S S A S N K F V F L

 AAAAATGAAGGGTTAATTGACTTATCATTTATGATAAATGCATGCTTATGACATAATT 1740
 K N E G L I D L S F M I N A C Y D I I I

 GAGGAAATGCCTTTCACCTTATATTGTCAGGGTGTGTTGACTGATGTTGTTCCATG 1800
 E G M P F S P Y I C A G V G T D V V S M

 TTTGAAGCTATAAAATCCTAAATTCTTACCAAGGAAAACTAGGATTAGGTTATAGTATA 1860
 F E A I N P K I S Y Q G K L G L G Y S I

 AGTCAGAACGCCTCTGTTTATCGGTGGACACTTTCACAGAGTCATAGGTTAATGAATT 1920
 S S E A S V F I G G H F R V I G N E F

 AGAGACATCCCTGCTATGGTTCCCTAGTGGATCAAATCTTCCAGAAAACCAATTGCAATA 1980
 R D I P A M V P S G S N L P E N Q F A I
 (SEQ ID NO: 5)

 GTAAACACTAAATGTTGTGTCACCTTGGCATAGAACCTGGAGGAAGATTAACTTCTGA 2031
 V T L N V C H F G I E L G R F N F *
 (SEQ ID NO: 6)

Fig. 7C

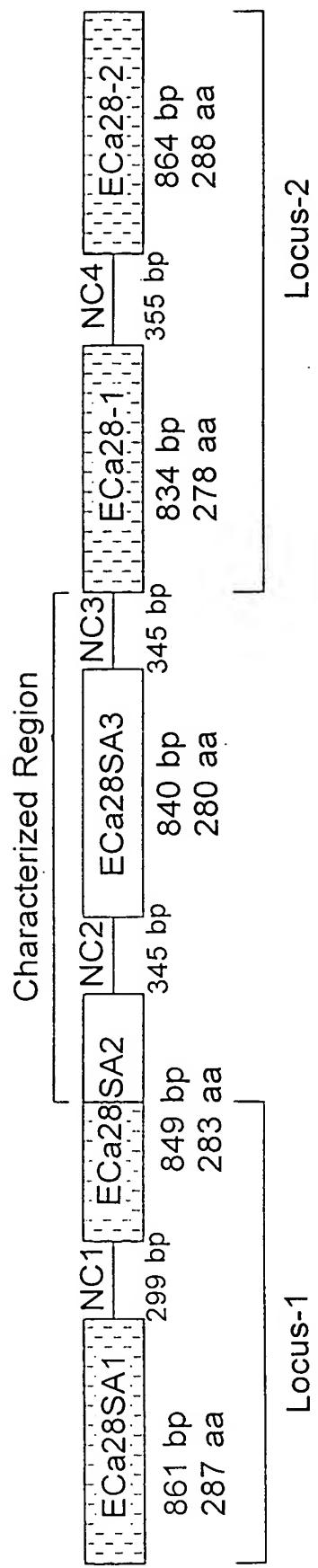


Fig. 8

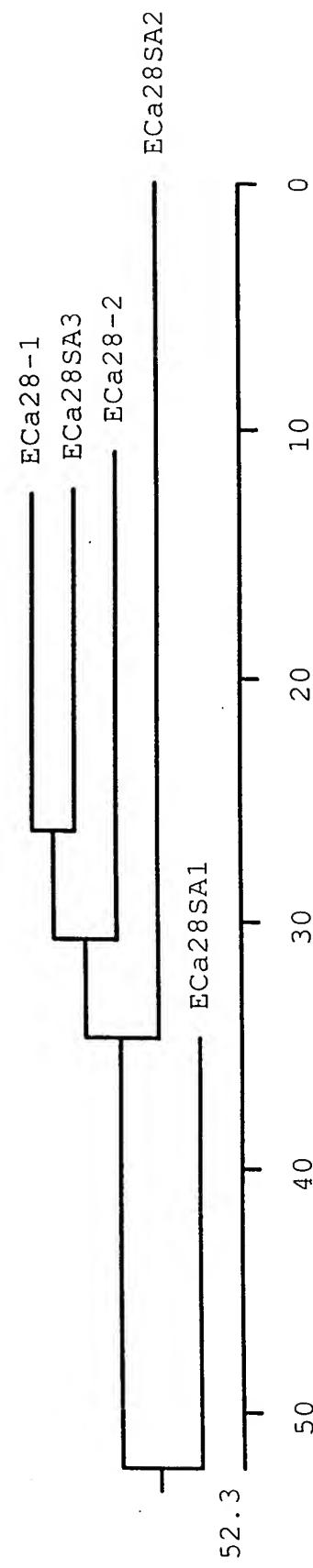


Fig. 9

1 TAATACTTCTATATGT-ACATGTTAAAATAGTACTAGTTGCTTCTGGTT--TATAAACGCAAGAGAGAA-- 28nc1
 1 ... TTCGTGG .A--C . . . A . C . CG . . -GC . . AA . T . G . TT . T . A . CTC . GC . G . . T . AAG . . A . A . . TA 28nc2
 1 .G . . TT . AT . G . . CC . . . A GA . CTA . AC . . T . . T . A . TA . . GC . . C . T . AA . . A . A . . AA 28nc3
 1 . . . TT . AT . G . . CC . . . A GA . CTA . AC . . T . . T . AWT A . . GC . . C . T . AA . . A . A . . AA 28nc4

70 ATAGT-----TAGTAATAAATTAGAAG-----TAAAGAAGT--TATT--AGAAAAGT-CA 28nc1
 72 G . . G . -AAAATTAC C . AC TGAC . . T . CAAGTTTAC C . . GCT . . . CTC . C . . . C . T . T 28nc2
 75 . . . GGCAAAAGAATG . . C GAGG . GGG . GGGGGAC . . . TT . . CCTTC--T . TTC . T . T 28nc3
 74 . . . GGCAAAAGAATG . . C GAGG . GGG . GGGGGAC C . . TT . . CCTTC--T . TGC . T . C 28nc4

112 TATGTTTTCATTTGTCATTGAT-ACTCAACTA-----AAAGTAGTAT-----AAATGT----- 28nc1
 136 .G . . C . . T . . CTCT--T . CA . - . G . . A . -GTAC . -CT . . CTC . CACTACTGTAG . G . . GTTTATCAATGC 28nc2
 139 A . . A . . C . . T . --ACT T . . . A . . GCAC . . CTC . A . GCTTCCA-GG-A . . . A . GT-TTCTAAATAT 28nc3
 138 C . A TCYC . CT . . . T . . G . . . T . . AC . . ACAG . G . . A . . CCTCACGG-A . . . CT . . ATCTCAAATAT 28nc4

159 --TACTTATAATAAT-TTTACGTAGTATATAATTTCCCTTACAAAAGGCCACTAGTATTTTATA 28nc1
 205 TT . GT --C . C . . A . . A . . G TT CT A 28nc2
 202 TT . . T CC . . . CC . . TA . . . A T AT . T . . A . G 28nc3
 211 TT . . T CC . . . CC . . C- . . TA . . . A T AT 28nc4

222 CTAAAGC-TATACCTGGCTTGTATTTAATTGTACTACTGTTAATTACTTT-TCACTGTT---TCT 28nc1
 269 .-T . G . ATA . . . T . C . . A GC . . . A . . C . . CC . . . T T A TA 28nc2
 268 . . T . . TATA . . . T . C C . . . C . C . . CC . . . T T A TA 28nc3
 276 .C- . . ATA . . . T . C . . A . . . CT . . . CT . . C . C . . C . . . T . T T . G . . . A . . AGG . TA 28nc4

-35

-10

292 GGTGTAAAT 28nc1 (SEQ ID NO: 30)
 338 28nc2 (SEQ ID NO: 31)
 339 28nc3 (SEQ ID NO: 32)
 339 TA-A . . -W 28nc4 (SEQ ID NO: 33)

RBS

Fig. 10

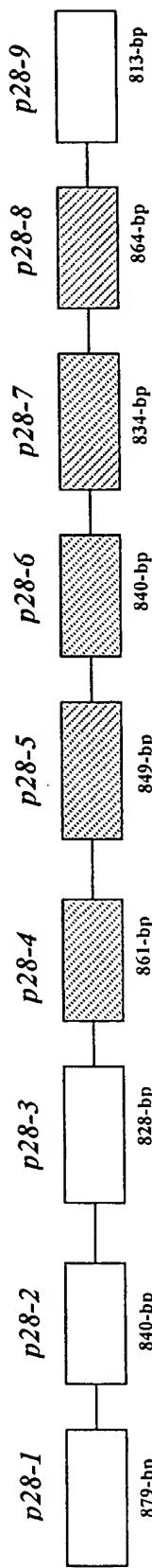


Fig. 11

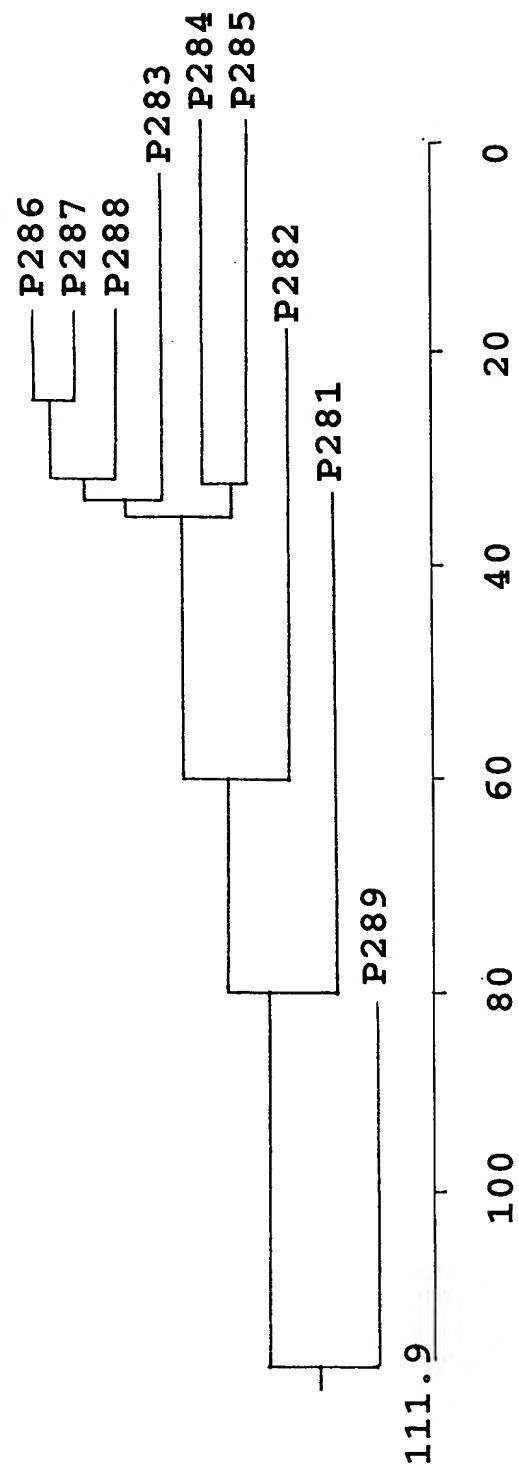


Fig. 12

ATGAATAATAAACTCAAATTACTATAATAAACACAGTATTAGTATGCTTATTGTCATTA 60
 M N N K L K F T I I N T V L V C L L S L

 CCTAATATATCTCCTCAAAGGCCATAAACATAACGCTAAAAAGTACTACGGATTATAT 120
 P N I S S S K A I N N N A K K Y Y G L Y

 ATCAGTGGACAATATAAACCCAGTGTTCAGTAATTTTCAGTTAAAGAAACC 180
 I S G Q Y K P S V S V F S N F S V K E T

 AATGTCATAACTAAAAACCTTATAGCTTAAAAAAAGATGTTGACTCTATTGAAACCAAG 240
 N V I T K N L I A L K K D V D S I E T K

 ACTGATGCCAGTGTAGGTATTAGTAACCCATCAAATTTACTATCCCCTATACAGCTGTA 300
 T D A S V G I S N P S N F T I P Y T A V

 TTTCAAGATAATTCTGTCAATTCAATGGAACTATTGGTTACACCTTGCTGAAGGTACA 360
 F Q D N S V N F N G T I G Y T F A E G T

 AGAGTTGAAATAGAAGGTTCTTATGAGGAATTGATGTTAAAAACCTGGAGGCTATACA 420
 R V E I E G S Y E E F D V K N P G G Y T

 CTAAGTGATGCCTATCGCTATTTGCATTAGCACGTGAAATGAAAGGTAATAGTTTACA 480
 L S D A Y R Y F A L A R E M K G N S F T

 CCTAAAGAAAAAGTTCTAATAGTATTTTACACTGTAATGAGAAATGATGGATTATCT 540
 P K E K V S N S I F H T V M R N D G L S

 ATAATATCTGTTATAGTAAATGTTGCTACGATTTCTCTTGAACAATTGTCAATATCG 600
 I I S V I V N V C Y D F S L N N L S I S

 CCTTACATATGTGGAGGAGCAGGGGTAGATGCTATAGAATTCTCGATGTATTACACATT 660
 P Y I C G G A G V D A I E F F D V L H I

 AAGTTGCATATCAAAGCAAGCTAGGTATTGCTTATTCTCTACCATCTAACATTAGTCTC 720
 K F A Y Q S K L G I A Y S L P S N I S L

 TTTGCTAGTTATATTACCATAAAGTAATGGGCAATCAATTAAAAATTAAATGTCCAA 780
 F A S L Y Y H K V M G N Q F K N L N V Q

 CATGTTGCTGAACCTGCAAGTATACTAAATTACATCCGCAGTTGCTACACTTAATATT 840
 H V A E L A S I P K I T S A V A T L N I

 GGTTATTTGGAGGTGAAATTGGTGCAAGATTGACATT (SEQ ID No. 39) 879
 G Y F G G E I G A R L T F (SEQ ID NO. 40)

Fig. 13

ATGAATTATAAGAAAATTCTAGTAAGAAGCGCGTTAATCTCATTAATGTCAATCTTACCA 60
 M N Y K K I L V R S A L I S L M S I L P
 TATCAGTCTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC 120
 Y Q S F A D P V G S R T N D N K E G F Y
 ATTAGTGCAAAAGTACAATCCAAGTATATCACACTTAGAAAATTCTCTGCTGAAGAACT 180
 I S A K Y N P S I S H F R K F S A E E T
 CCTATTAAATGGAACAAATTCTCTCACTAAAAAGTTTCGGACTAAAGAAAGATGGTGAT 240
 P I N G T N S L T K K V F G L K K D G D
 ATAACAAAAAAAGACGATTTACAAGAGTAGCTCCAGGCATTGATTTCAAAATAACTTA 300
 I T K K D D F T R V A P G I D F Q N N L
 ATATCAGGATTTCAGGAAGTATTGGTTACTCTATGGACGGACCAAGAATAGAACTTGAA 360
 I S G F S G S I G Y S M D G P R I E L E
 GCTGCATATCAACAATTAAATCCAAAAACACCGATAACAAATGATACTGATAATGGTGAA 420
 A A Y Q Q F N P K N T D N N D T D N G E
 TACTATAAACATTTCGATTATCTCGTAAAGATGCAATGGAAGATCAGCAATATGTAGTA 480
 Y Y K H F A L S R K D A M E D Q Q Y V V
 CTTAAAAATGACGGCATAACTTTATGTCATTGATGGTTAATACTGCTATGACATTACA 540
 L K N D G I T F M S L M V N T C Y D I T
 GCTGAAGGAGTATCTTCGTACCATATGCATGTGCAGGTATAGGAGCAGATCTTACT 600
 A E G V S F V P Y A C A G I G A D L I T
 ATTTTAAAGACCTCAATCTAAAATTGCTTACCAAGGAAAATAGGTATTAGTTACCT 660
 I F K D L N L K F A Y Q G K I G I S Y P
 ATCACACCAGAAGTCTCTGCATTATTGGTGGATACTACCATGGCGTTATTGGTAATAAA 720
 I T P E V S A F I G G Y Y H G V I G N K
 TTTGAGAAGATACTGTAATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACATCT 780
 F E K I P V I T P V V L N D A P Q T T S
 GCTTCAGTAACTCTGACGTTGGATACTTGGCGGAGAAATTGGAATGAGGTTCACCTTC 840
 (SEQ ID No. 41)
 A S V T L D V G Y F G G E I G M R F T F
 (SEQ ID No. 42)

Fig. 14